f. Young

PCT *09*

RAW SEQUENCE LISTING   DATE: 05/29/2001
PATENT APPLICATION: US/09/762,194   TIME: 15:53:16

Input Set : **A:\Seqlist.txt**
Output Set: **C:\CRF3\05292001\I762194.raw**

ENTERED

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 4 <110> APPLICANT: Elbaz, Nathalie
 5         Nahmias, Clara
 6         Strosberg, Arthur Donny
 8 <120> TITLE OF INVENTION: NUCLEIC SEQUENCES ENCODING AN AT2
 9         RECEPTOR-INTERACTING PROTEIN (ATIP) AND THEIR APPLICATIONS
13 <130> FILE REFERENCE: 33339/208804
15 <140> CURRENT APPLICATION NUMBER: US 09/762,194
16 <141> CURRENT FILING DATE: 2001-04-19
18 <150> PRIOR APPLICATION NUMBER: PCT/FR99/01908
19 <151> PRIOR FILING DATE: 1999-08-02
21 <150> PRIOR APPLICATION NUMBER: FR 98/09997
22 <151> PRIOR FILING DATE: 1998-08-04
24 <160> NUMBER OF SEQ ID NOS: 12
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1803
30 <212> TYPE: DNA
31 <213> ORGANISM: Mus musculus
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (178)...(1500)
37 <400> SEQUENCE: 1
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39 ttttctctgg ctgtatctct tggcctggaa gaaccccgag ttgccaagag acacagtatg     120
40 tgatggtccc tggaaaagct gcttcccctg cgaagttctc ccactggctt cgaagac atg     180
41                                                                   Met
42                                                                     1
44 ctg ttg tct ccc aaa ttc tcc tta tcc acc atc cac gtc cgc cta acc     228
45 Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu Thr
46              5                  10                  15
48 gcc aaa gga ctg ctt cga aac ctc cgg ctt cct tcg ggg ctc agg aaa     276
49 Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg Lys
50          20                  25                  30
52 aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat ccc     324
53 Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn Pro
54      35                  40                  45
56 agg agc ctg tgc atc cag acc cag aca gct cca gat gtg ctg tcc tcc     372
57 Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser Ser
58  50                  55                  60                  65
60 gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc caa     420
61 Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser Gln
62                  70                  75                  80
64 agt gga ttc atc ctg cac ctc agg cag ctt ctt tcc cgt ggt aac aac     468
65 Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn Asn
66              85                  90                  95
68 aag ttt gaa gcg ctg aca gtt gtg atc cag cac ctc ctg tct gag cgg     516
69 Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg
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70          100                105                110
72 gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc agc      564
73 Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Ser
74     115                120                125
76 ctc cgg gga gag cta gtt gct gct tca agc gcc tgt gag aag cta gaa      612
77 Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu Glu
78 130                135                140                145
80 aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag aaa      660
81 Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln Lys
82             150                155                160
84 cta aac cag cag cat cag aca gac cgg acg gaa ctg gag aac cgg ctg      708
85 Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu
86             165                170                175
88 aag gac tta tac acc gca gag tgt gag aag ctt cag agc att tac att      756
89 Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile
90             180                185                190
92 gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac aac      804
93 Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn
94     195                200                205
96 tta aac gcc gcc cat gag acc act aag ctt gag att gaa gct agc cac      852
97 Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His
98 210                215                220                225
100 tcg gag aag gtg gaa ttg ctg aag aag acc tat gaa acc tcc ctt tca     900
101 Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser
102             230                235                240
104 gaa atc aag aag agc cat gag atg gag aag aag tca ctg gag gat ctg     948
105 Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu
106             245                250                255
108 ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg aag     996
109 Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys
110             260                265                270
112 agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa aag    1044
113 Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln Lys
114     275                280                285
116 caa ctg tca aga gag aag gcg aat tcc aaa aac cct cag gtc atg tat    1092
117 Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met Tyr
118 290                295                300                305
120 ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag aat    1140
121 Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn
122             310                315                320
124 gag aag ctg cac cag cag gac atg aag cta atg aag atg gaa aag ctg    1188
125 Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys Leu
126             325                330                335
128 gtg gac aat aac aca gca ttg gtt gac aag ctg aag cga ttc cag cag    1236
129 Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln
130             340                345                350
132 gaa aac gag gag tta aaa gct cgc atg gac aaa cac atg gca att tca    1284
133 Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser
134     355                360                365
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136 agg caa ctt tcc acc gag cag gcc gcg ctg caa gag tcc ctt gag aag    1332
137 Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu Lys
138 370              375              380              385
140 gag tca aag gtc aac aag aga ctg tcc atg gag aac gag gaa ctt ctg    1380
141 Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu
142              390              395              400
144 tgg aaa ctg cac aac gga gac ctg tgc agc ccc aag aga tcc ccc acc    1428
145 Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr
146              405              410              415
148 tcc tcg gcc atc cct ttc cag tcc ccc agg aat tct ggt tcc ttc tcc    1476
149 Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe Ser
150              420              425              430
152 agc ccc agc atc tca ccc aga tga'cggcttctga acgcaggaga ctctctgaag    1530
153 Ser Pro Ser Ile Ser Pro Arg  *
154              435              440
156 gcactgaggt gcgcttctgc aggactgacc ctctcatggg aactcgagtt gctgcgttag    1590
157 ctctctggaa tatccccagg atatcgggag agcagccgcc aaccgtatca gctacgtacg    1650
158 aatagagagc tccaatagaa gacttttaac ttggtccaaa agcctcctcc aaaaacagat    1710
159 ttcggaactg aagtggacat agttgcacaa agcacttacg gaacgaggga accttgttct    1770
160 ttgccttcct tcacctaagc ataggctttc cag                                1803
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162 <210> SEQ ID NO: 2
163 <211> LENGTH: 440
164 <212> TYPE: PRT
165 <213> ORGANISM: Mus musculus
167 <400> SEQUENCE: 2

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168 Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu
169 1               5                10               15
170 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg
171              20               25               30
172 Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
173              35               40               45
174 Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
175      50               55               60
176 Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
177 65               70               75               80
178 Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
179              85               90               95
180 Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
181              100              105              110
182 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
183      115              120              125
184 Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
185      130              135              140
186 Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
187 145              150              155              160
188 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
189              165              170              175
190 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
191              180              185              190
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192 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
193         195                 200             205
194 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
195     210             215                 220
196 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
197 225             230                 235                 240
198 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
199         245             250                 255
200 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
201         260             265                 270
202 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
203     275             280                 285
204 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
205     290             295                 300
206 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
207 305             310                 315                 320
208 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
209         325             330                 335
210 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
211     340             345             .       350
212 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
213     355             360                 365
214 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
215     370             375                 380
216 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
217 385         .       390                 395                 400
218 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
219             405             410                 415
220 Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
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223         435             440
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226 <211> LENGTH: 1323
227 <212> TYPE: DNA
228 <213> ORGANISM: Mus musculus
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (1)...(1323)
234 <400> SEQUENCE: 3
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237 1               5                   10                  15
239 acc gcc aaa gga ctg ctt cga aac ctc cgg ctt cct tcg ggg ctc agg       96
240 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg
241             20                  25                  30
243 aaa aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat      144
244 Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
245         35                  40                  45
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247 ccc agg agc ctg tgc atc cag acc cag aca gct cca gat gtg ctg tcc     192
248 Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
249     50                  55                  60
251 tcc gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc     240
252 Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
253 65                  70                  75                  80
255 caa agt gga ttc atc ctg cac ctc agg cag ctt ctt tcc cgt ggt aac     288
256 Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
257             85                  90                  95
259 aac aag ttt gaa gcg ctg aca gtt gtg atc cag cac ctc ctg tct gag     336
260 Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
261             100                 105                 110
263 cgg gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc     384
264 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
265         115                 120                 125
267 agc ctc cgg gga gag cta gtt gct gct tca agc gcc tgt gag aag cta     432
268 Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
269     130                 135                 140
271 gaa aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag     480
272 Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
273 145                 150                 155                 160
275 aaa cta aac cag cag cat cag aca gac cgg acg gaa ctg gag aac cgg     528
276 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
277             165                 170                 175
279 ctg aag gac tta tac acc gca gag tgt gag aag ctt cag agc att tac     576
280 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
281             180                 185                 190
283 att gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac     624
284 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
285         195                 200                 205
287 aac tta aac gcc gcc cat gag acc act aag ctt gag att gaa gct agc     672
288 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
289     210                 215                 220
291 cac tcg gag aag gtg gaa ttg ctg aag aag acc tat gaa acc tcc ctt     720
292 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
293 225                 230                 235                 240
295 tca gaa atc aag aag agc cat gag atg gag aag aag tca ctg gag gat     768
296 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
297             245                 250                 255
299 ctg ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg     816
300 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
301             260                 265                 270
303 aag agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa     864
304 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
305         275                 280                 285
307 aag caa ctg tca aga gag aag gcg aat tcc aaa aac cct cag gtc atg     912
308 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
309     290                 295                 300
311 tat ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag     960
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VERIFICATION SUMMARY   DATE: 05/29/2001
PATENT APPLICATION: **US/09/762,194**   TIME: 15:53:17

Input Set : **A:\Seqlist.txt**
Output Set: **C:\CRF3\05292001\I762194.raw**

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date